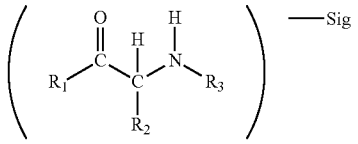

wherein R_1 is an OH or an amino acid or acids and R_2 is an amino acid side chain and R_3 is H or an amino acid or acids and Sig is attached to the R_1 and/or R_2 and/or R_3.

The invention claimed is:

1. A process for detecting a nucleic acid of interest in a sample, which process comprises:

(A) providing a sample which may contain a nucleic acid of interest;

(B) providing:

(i) an oligo- or polynucleotide that comprises two segments, the first segment comprising a nucleotide sequence that is complementary to and capable of specifically hybridizing to and forming a hybrid with said nucleic acid of interest or a portion thereof, and the second segment comprising an operator sequence that is capable of binding to or complexing with a non-radioactively detectable protein; and

(ii) a non-radioactively detectable protein which is non-radioactive and has a binding affinity to said operator sequence;

(C) contacting a sample suspected of containing said nucleic acid of interest with said oligo- or polynucleotide (i) and said non-radioactively detectable protein (ii) to form a complex; and

(D) detecting non-radioactively the presence of said non-radioactively detectable protein in said complex to detect said nucleic acid of interest.

2. The process according to claim **1**, wherein the nucleic acid of interest comprises DNA, RNA or a DNA-RNA hybrid.

3. The process according to claim **1**, wherein the nucleic acid of interest is double-stranded or single-stranded.

4. The process according to claim **1**, wherein the nucleic acid of interest has been rendered single-stranded.

5. The process according to claim **1**, wherein the nucleic acid of interest is derived from an organism.

6. The process according to claim **5**, wherein the organism comprises prokaryotes or eukaryotes.

7. The process according to claim **5**, wherein said organism bacteria, fungi, viruses, yeast or mammals.

8. The process according to claim **5**, wherein said organism is living.

9. The process according to claim **1**, wherein the sample is suspected of containing an etiological agent and the nucleic acid of interest is naturally associated with the etiological agent.

10. The process according to claim **9**, wherein the sample is of human or animal origin and the etiological agent comprises bacteria, virus or fungi.

11. The process according to claim **1**, wherein said nucleic acid of interest is derived from an organism comprising *Streptococcus pyrogenes, Neisseria meningitides, Staphylococcus aureus, Candida albicans, Pseudomonas aeruginosa, Neisseria gonorrhoeae*, or *Mycobacterium tuberculosis*.

12. The process according to claim **1**, wherein said one or more oligo- or polynucleotides are derived from *Neisseria gonorrhoeae* sequences.

13. The process according to claim **1**, wherein the sample comprises a bacterium suspected of containing a nucleic acid of interest which imparts resistance to an antibiotic and wherein the oligo- or polynucleotide comprises a polynucleotide complementary to the sequence of the bacterium which confers resistance to the antibiotic.

14. The process according to claim **13**, wherein when said bacterium is *Streptococcus pyrogenes* or *Neisseria meningtidis*, said antibiotic is penicillin, wherein when said bacterium is *Staphylococcus aureus, Candida albicans, Pseudomonas aeruginosa, Streptococcus pyrogenes*, or *Neisseria gonorrhoea*, said antibiotic is a tetracycline, and wherein when said bacterium is *Mycobacterium tuberculosis*, said antibiotic is an aminoglycoside.

15. The process according to claim **14**, wherein said bacterium is *Neisseria gonorrhoeae* and said antibiotic comprises penicillin, tetracycline, aminoglycoside or combinations thereof.

16. The process according to claim **1**, wherein the sample is suspected of containing a nucleic acid of interest associated with a genetic disorder and wherein the oligo- or polynucleotide comprises a polynucleotide complementary to the nucleic acid associated with the genetic disorder.

17. The process according to claim **1**, wherein said sample is suspected of containing a nucleic acid of interest associated with thalassemia and wherein the oligo- or polynucleotide comprises a polynucleotide complementary to the nucleic acid which is absent in the thalassemic subjects.

18. The process according to claim **1**, wherein said process is utilized for chromosomal karyotyping which comprises contacting the sample with a series of the oligo- or polynucleotides (i) which are complementary to a series of known genetic sequences located on chromosomes.

19. The process according to claim **1**, wherein said process is utilized to determine the number of copies of an individual chromosome in a sample.

20. The process according to claim **1**, wherein said non-radioactive detectable protein comprises an antibody, a promoter, a repressor or an inducer.

21. The process according to claim **20**, wherein said repressor comprises a lac repressor.

22. The process according to claim **20**, wherein said operator sequence is covalently attached to said oligo- or polynucleotide.

23. The process according to claim **22**, wherein said covalent attachment has been carried out by ligation.

24. The process according to claim **22**, wherein said covalent attachment does not interfere substantially with the characteristic ability of said non-radioactively detectable protein to bind to any hybrid formed between said oligo- or polynucleotide and said nucleic acid of interest.

25. The process according to claim **22**, wherein said covalent attachment does not interfere substantially with the characteristic ability of said non-radioactively detectable protein to be detected non-radioactively when bound to any hybrid formed between said oligo- or polynucleotide and said nucleic acid of interest.

26. The process according to claim **22**, wherein said operator sequence is attached via a covalent attachment by an olefinic bond at the α-position relative to the point of attachment to said nucleotide structure or nucleotide analog structure (i), a CH_2NH— moiety, or both.

27. The process according to claim **26**, wherein said covalent attachment comprises an allylamine group.

28. The process according to claim **26**, wherein said covalent attachment comprises or includes an olefinic bond at the α-position relative to the point of attachment to the nucleotide, or any of the moieties